



SEQUENCE LISTING

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YAMADA, KAZUYA

<120> TRANSCRIPTIONAL REGULATOR ZHX3

<130> 47232.5003/00US

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<150> JP 2002-366512

<151> 2002-12-18

<160> 36

<170> PatentIn Ver. 3.3

<210> 1

<211> 956

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Ser Lys Arg Lys Ser Thr Thr Pro Cys Met Ile Pro Val Lys
1 5 10 15

Thr Val Val Leu Gln Asp Ala Ser Met Glu Ala Gln Pro Ala Glu Thr
20 25 30

Leu Pro Glu Gly Pro Gln Gln Asp Leu Pro Pro Glu Ala Ser Ala Ala
35 40 45

Ser Ser Glu Ala Ala Gln Asn Pro Ser Ser Thr Asp Gly Ser Thr Leu
50 55 60

Ala Asn Gly His Arg Ser Thr Leu Asp Gly Tyr Leu Tyr Ser Cys Lys
65 70 75 80

Tyr Cys Asp Phe Arg Ser His Asp Met Thr Gln Phe Val Gly His Met
85 90 95

Asn Ser Glu His Thr Asp Phe Asn Lys Asp Pro Thr Phe Val Cys Ser
100 105 110

Gly Cys Ser Phe Leu Ala Lys Thr Pro Glu Gly Leu Ser Leu His Asn
115 120 125

Ala Thr Cys His Ser Gly Glu Ala Ser Phe Val Trp Asn Val Ala Lys
130 135 140

Pro Asp Asn His Val Val Val Glu Gln Ser Ile Pro Glu Ser Thr Ser
145 150 155 160

Thr	Pro	Asp	Leu	Ala	Gly	Glu	Pro	Ser	Ala	Glu	Gly	Ala	Asp	Gly	Gln	165	170	175
Ala	Glu	Ile	Ile	Ile	Thr	Lys	Thr	Pro	Ile	Met	Lys	Ile	Met	Lys	Gly	180	185	190
Lys	Ala	Glu	Ala	Lys	Lys	Ile	His	Thr	Leu	Lys	Glu	Asn	Val	Pro	Ser	195	200	205
Gln	Pro	Val	Gly	Glu	Ala	Leu	Pro	Lys	Leu	Ser	Thr	Gly	Glu	Met	Glu	210	215	220
Val	Arg	Glu	Gly	Asp	His	Ser	Phe	Ile	Asn	Gly	Ala	Val	Pro	Val	Ser	225	230	235
Gln	Ala	Ser	Ala	Ser	Ser	Ala	Lys	Asn	Pro	His	Ala	Ala	Asn	Gly	Pro	245	250	255
Leu	Ile	Gly	Thr	Val	Pro	Val	Leu	Pro	Ala	Gly	Ile	Ala	Gln	Phe	Leu	260	265	270
Ser	Leu	Gln	Gln	Gln	Pro	Pro	Val	His	Ala	Gln	His	His	Val	His	Gln	275	280	285
Pro	Leu	Pro	Thr	Ala	Lys	Ala	Leu	Pro	Lys	Val	Met	Ile	Pro	Leu	Ser	290	295	300
Ser	Ile	Pro	Thr	Tyr	Asn	Ala	Ala	Met	Asp	Ser	Asn	Ser	Phe	Leu	Lys	305	310	315
Asn	Ser	Phe	His	Lys	Phe	Pro	Tyr	Pro	Thr	Lys	Ala	Glu	Leu	Cys	Tyr	325	330	335
Leu	Thr	Val	Val	Thr	Lys	Tyr	Pro	Glu	Glu	Gln	Leu	Lys	Ile	Trp	Phe	340	345	350
Thr	Ala	Gln	Arg	Leu	Lys	Gln	Gly	Ile	Ser	Trp	Ser	Pro	Glu	Glu	Ile	355	360	365
Glu	Asp	Ala	Arg	Lys	Lys	Met	Phe	Asn	Thr	Val	Ile	Gln	Ser	Val	Pro	370	375	380
Gln	Pro	Thr	Ile	Thr	Val	Leu	Asn	Thr	Pro	Leu	Val	Ala	Ser	Ala	Gly	385	390	395
Asn	Val	Gln	His	Leu	Ile	Gln	Ala	Ala	Leu	Pro	Gly	His	Val	Val	Gly	405	410	415
Gln	Pro	Glu	Gly	Thr	Gly	Gly	Gly	Leu	Leu	Val	Thr	Gln	Pro	Leu	Met	420	425	430
Ala	Asn	Gly	Leu	Gln	Ala	Thr	Ser	Ser	Pro	Leu	Pro	Leu	Thr	Val	Thr	435	440	445
Ser	Val	Pro	Lys	Gln	Pro	Gly	Val	Ala	Pro	Ile	Asn	Thr	Val	Cys	Ser	450	455	460

Asn	Thr	Thr	Ser	Ala	Val	Lys	Val	Val	Asn	Ala	Ala	Gln	Ser	Leu	Leu	465	470	475	480
Thr	Ala	Cys	Pro	Ser	Ile	Thr	Ser	Gln	Ala	Phe	Leu	Asp	Ala	Ser	Ile	485	490	495	
Tyr	Lys	Asn	Lys	Lys	Ser	His	Glu	Gln	Leu	Ser	Ala	Leu	Lys	Gly	Ser	500	505	510	
Phe	Cys	Arg	Asn	Gln	Phe	Pro	Gly	Gln	Ser	Glu	Val	Glu	His	Leu	Thr	515	520	525	
Lys	Val	Thr	Gly	Leu	Ser	Thr	Arg	Glu	Val	Arg	Lys	Trp	Phe	Ser	Asp	530	535	540	
Arg	Arg	Tyr	His	Cys	Arg	Asn	Leu	Lys	Gly	Ser	Arg	Ala	Met	Ile	Pro	545	550	555	560
Gly	Asp	His	Ser	Ser	Ile	Ile	Ile	Asp	Ser	Val	Pro	Glu	Val	Ser	Phe	565	570	575	
Ser	Pro	Ser	Ser	Lys	Val	Pro	Glu	Val	Thr	Cys	Ile	Pro	Thr	Thr	Ala	580	585	590	
Thr	Leu	Ala	Thr	His	Pro	Ser	Ala	Lys	Arg	Gln	Ser	Trp	His	Gln	Thr	595	600	605	
Pro	Asp	Phe	Thr	Pro	Thr	Lys	Tyr	Lys	Glu	Arg	Ala	Pro	Glu	Gln	Leu	610	615	620	
Arg	Ala	Leu	Glu	Ser	Ser	Phe	Ala	Gln	Asn	Pro	Leu	Pro	Leu	Asp	Glu	625	630	635	640
Glu	Leu	Asp	Arg	Leu	Arg	Ser	Glu	Thr	Lys	Met	Thr	Arg	Arg	Glu	Ile	645	650	655	
Asp	Ser	Trp	Phe	Ser	Glu	Arg	Arg	Lys	Lys	Val	Asn	Ala	Glu	Glu	Thr	660	665	670	
Lys	Lys	Ala	Glu	Glu	Asn	Ala	Ser	Gln	Glu	Glu	Glu	Glu	Ala	Ala	Glu	675	680	685	
Asp	Glu	Gly	Gly	Glu	Glu	Asp	Leu	Ala	Ser	Glu	Leu	Arg	Val	Ser	Gly	690	695	700	
Glu	Asn	Gly	Ser	Leu	Glu	Met	Pro	Ser	Ser	His	Ile	Leu	Ala	Glu	Arg	705	710	715	720
Lys	Val	Ser	Pro	Ile	Lys	Ile	Asn	Leu	Lys	Asn	Leu	Arg	Val	Thr	Glu	725	730	735	
Ala	Asn	Gly	Arg	Asn	Glu	Ile	Pro	Gly	Leu	Gly	Ala	Cys	Asp	Pro	Glu	740	745	750	
Asp	Asp	Glu	Ser	Asn	Lys	Leu	Ala	Glu	Gln	Leu	Pro	Gly	Lys	Val	Ser	755	760	765	

Cys Lys Lys Thr Ala Gln Gln Arg His Leu Leu Arg Gln Leu Phe Val
 770 775 780

Gln Thr Gln Trp Pro Ser Asn Gln Asp Tyr Asp Ser Ile Met Ala Gln
 785 790 795 800

Thr Gly Leu Pro Arg Pro Glu Val Val Arg Trp Phe Gly Asp Ser Arg
 805 810 815

Tyr Ala Leu Lys Asn Gly Gln Leu Lys Trp Tyr Glu Asp Tyr Lys Arg
 820 825 830

Gly Asn Phe Pro Pro Gly Leu Leu Val Ile Ala Pro Gly Asn Arg Glu
 835 840 845

Leu Leu Gln Asp Tyr Tyr Met Thr His Lys Met Leu Tyr Glu Glu Asp
 850 855 860

Leu Gln Asn Leu Cys Asp Lys Thr Gln Met Ser Ser Gln Gln Val Lys
 865 870 875 880

Gln Trp Phe Ala Glu Lys Met Gly Glu Glu Thr Arg Ala Val Ala Asp
 885 890 895

Thr Gly Ser Glu Asp Gln Gly Pro Gly Thr Gly Glu Leu Thr Ala Val
 900 905 910

His Lys Gly Met Gly Asp Thr Tyr Ser Glu Val Ser Glu Asn Ser Glu
 915 920 925

Ser Trp Glu Pro Arg Val Pro Glu Ala Ser Ser Glu Pro Phe Asp Thr
 930 935 940

Ser Ser Pro Gln Ala Gly Arg Gln Leu Glu Thr Asp
 945 950 955

<210> 2

<211> 522

<212> PRT

<213> Rattus norvegicus

<400> 2

Cys Ser Phe Leu Ala Lys Thr Pro Glu Gly Leu Ser Leu His Asn Ala
 1 5 10 15

Lys Cys His Ser Gly Glu Ala Ser Phe Leu Trp Asn Val Thr Lys Pro
 20 25 30

Asp Asn His Val Val Val Glu Gln Ser Val Pro Glu Asn Ala Ser Ser
 35 40 45

Ser Val Leu Ala Gly Glu Ser Thr Glu Gly Thr Glu Ile Ile Ile Thr
 50 55 60

Lys Thr Pro Ile Met Lys Ile Met Lys Gly Lys Ala Glu Ala Lys Lys
 65 70 75 80

Ile	His	Met	Leu	Lys	Glu	Asn	Ala	Pro	Thr	Gln	Pro	Gly	Gly	Glu	Ala	85	90	95
Leu	Pro	Lys	Pro	Leu	Ala	Gly	Glu	Thr	Glu	Gly	Lys	Glu	Gly	Asp	His	100	105	110
Thr	Phe	Ile	Asn	Gly	Ala	Thr	Pro	Val	Ser	Gln	Ala	Ser	Ala	Asn	Ser	115	120	125
Thr	Lys	Pro	Pro	His	Thr	Ala	Asn	Gly	Pro	Leu	Ile	Gly	Thr	Val	Pro	130	135	140
Val	Leu	Pro	Ala	Gly	Ile	Ala	Gln	Phe	Leu	Ser	Leu	Gln	Gln	Pro	Thr	145	150	155
Val	His	Pro	Gln	His	His	Pro	His	Gln	Pro	Leu	Pro	Thr	Ser	Lys	Ala	165	170	175
Leu	Pro	Lys	Val	Met	Ile	Pro	Leu	Ser	Ser	Ile	Pro	Thr	Tyr	Asn	Ala	180	185	190
Ala	Met	Asp	Ser	Asn	Ser	Phe	Leu	Lys	Asn	Ser	Phe	His	Lys	Phe	Pro	195	200	205
Tyr	Pro	Thr	Lys	Ala	Glu	Leu	Cys	Tyr	Leu	Thr	Val	Val	Thr	Lys	Tyr	210	215	220
Pro	Glu	Glu	Gln	Leu	Lys	Ile	Trp	Phe	Thr	Ala	Gln	Arg	Leu	Lys	Gln	225	230	235
Gly	Ile	Ser	Trp	Ser	Pro	Glu	Glu	Ile	Glu	Asp	Ala	Arg	Lys	Lys	Met	245	250	255
Phe	Asn	Thr	Val	Ile	Gln	Ser	Val	Pro	Gln	Pro	Thr	Ile	Thr	Val	Leu	260	265	270
Asn	Thr	Pro	Leu	Val	Ala	Ser	Ala	Gly	Asn	Val	Gln	His	Leu	Ile	Gln	275	280	285
Ala	Ala	Leu	Pro	Gly	His	Ala	Val	Gly	Gln	Pro	Glu	Gly	Thr	Ala	Gly	290	295	300
Gly	Leu	Leu	Val	Thr	Gln	Pro	Leu	Met	Ala	Asn	Gly	Leu	Gln	Ala	Ser	305	310	315
Ser	Ser	Ser	Leu	Pro	Leu	Thr	Thr	Ala	Ser	Val	Pro	Lys	Pro	Thr	Ala	325	330	335
Ala	Pro	Ile	Asn	Thr	Val	Cys	Ser	Asn	Thr	Thr	Ser	Ala	Val	Lys	Val	340	345	350
Val	Asn	Ala	Ala	Gln	Ser	Leu	Leu	Thr	Ala	Cys	Pro	Ser	Ile	Thr	Ser	355	360	365
Gln	Ala	Phe	Leu	Asp	Ala	Asn	Ile	Tyr	Lys	Asn	Lys	Lys	Ser	His	Glu	370	375	380

Gln Leu Ser Ala Leu Lys Gly Ser Phe Cys Arg Asn Gln Phe Pro Gly
 385 390 395 400

Gln Ser Glu Val Glu His Leu Thr Lys Val Thr Gly Leu Ser Thr Arg
 405 410 415

Glu Val Arg Lys Trp Phe Ser Asp Arg Arg Tyr His Cys Arg Asn Leu
 420 425 430

Lys Gly Thr Arg Ala Met Val Pro Gly Glu His Gly Ser Val Leu Ile
 435 440 445

Asp Ser Val Pro Glu Val Pro Phe Pro Leu Ser Ser Lys Val Pro Glu
 450 455 460

Val Pro Cys Val Pro Thr Ala Thr Ser Leu Val Ser His Pro Ala Thr
 465 470 475 480

Lys Arg Gln Ser Trp His Gln Thr Pro Asp Phe Thr Pro Thr Lys Tyr
 485 490 495

Lys Glu Arg Ala Pro Glu Gln Leu Arg Val Leu Glu Ser Ser Phe Ala
 500 505 510

Gln Asn Pro Leu Pro Pro Glu Glu Glu Leu
 515 520

<210> 3

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 3

agcttcccga attctgcag

19

<210> 4

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 4

tcgactgcag aattcggga

19

<210> 5

<211> 19

<212> DNA

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 5
gtggcagaca caggcagtg 19

<210> 6
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 6
ggccg gatcc cagactggcc agtcc 25

<210> 7
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 7
cctgagcagc attccaacg 19

<210> 8
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 8
cttcttggtc tcctcagcat tcac 24

<210> 9
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 9
gtgattgtca ccatggccag 20

<210> 10
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 10
gaaggagttc ttcaggaagc 20

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 11
ccgggaattc ctgagcagca ttccaacgta 30

<210> 12
<211> 28
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 12
ccggggatcc agcccttcaa gttccggc 28

<210> 13
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 13
ccggggatcc agatttctta tttttgtaga tgc 33

<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 14
ccggaattc tcccctgagg agattgagg 29

<210> 15
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15
ccggaattc tacaaaaata agaaatctca tgaac 35

<210> 16
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 16
ccgggatcc ggaccagctg atcccctg 28

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 17
gtgggctgag gcacagactg 20

<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18

ccaatcatga agataatgaa aggc

24

<210> 19

<211> 10

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19

aattcccggg

10

<210> 20

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 20

gatcccggg

9

<210> 21

<211> 12

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21

tatggaattc gc

12

<210> 22

<211> 14

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 22

catggcgaat tcca

14

<210> 23
<211> 28
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 23
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28

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 24
ccgggaattc atggccagca agaggaaatc

30

<210> 25
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 25
ccgggggatcc caggggggatc atcactttg

29

<210> 26
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 26
ccgggggatcc tggcttggcc acgttccac

29

<210> 27
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 27
ccggggatcc tggcttggcc acgttcac 29

<210> 28
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 28
ccggggatcc tgggtcttta ttaaagctctg tg 32

<210> 29
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 29
ccgggaattc acctttgtat gcagtgggtg 30

<210> 30
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 30
ccgggaattc acctttgtat gcagtgggtg 30

<210> 31
<211> 30
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 31
 ccggaattc acctttgtat gcagtgggtg 30

<210> 32
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
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<400> 32
 ccggaattc acctttgtat gcagtgggtg 30

<210> 33
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
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<400> 33
 aattccacca cactggatcc ctggtac 27

<210> 34
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
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<400> 34
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<210> 35
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<400> 35
 catgcatggt gtggtggatt tcctc 25

<210> 36
 <211> 873
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Ala Ser Arg Arg Lys Ser Thr Thr Pro Cys Met Val Leu Ala Ser
 1 5 10 15
 Glu Gln Asp Pro Asp Leu Glu Leu Ile Ser Asp Leu Asp Glu Gly Pro
 20 25 30
 Pro Val Leu Thr Pro Val Glu Asn Thr Arg Ala Glu Ser Ile Ser Ser
 35 40 45
 Asp Glu Glu Val His Glu Ser Val Asp Ser Asp Asn Gln Gln Asn Lys
 50 55 60
 Lys Val Glu Gly Gly Tyr Glu Cys Lys Tyr Cys Thr Phe Gln Thr Pro
 65 70 75 80
 Asp Leu Asn Met Phe Thr Phe His Val Asp Ser Glu His Pro Asn Val
 85 90 95
 Val Leu Asn Ser Ser Tyr Val Cys Val Glu Cys Asn Phe Leu Thr Lys
 100 105 110
 Arg Tyr Asp Ala Leu Ser Glu His Asn Leu Lys Tyr His Pro Gly Glu
 115 120 125
 Glu Asn Phe Lys Leu Thr Met Val Lys Arg Asn Asn Gln Thr Ile Phe
 130 135 140
 Glu Gln Thr Ile Asn Asp Leu Thr Phe Asp Gly Ser Phe Val Lys Glu
 145 150 155 160
 Glu Asn Ala Glu Gln Ala Glu Ser Thr Glu Val Ser Ser Ser Gly Ile
 165 170 175
 Ser Ile Ser Lys Thr Pro Ile Met Lys Met Met Lys Asn Lys Val Glu
 180 185 190
 Asn Lys Arg Ile Ala Val His His Asn Ser Val Glu Asp Val Pro Glu
 195 200 205
 Glu Lys Glu Asn Glu Ile Lys Pro Asp Arg Glu Glu Ile Val Glu Asn
 210 215 220
 Pro Ser Ser Ser Ala Ser Glu Ser Asn Thr Ser Thr Ser Ile Val Asn
 225 230 235 240
 Arg Ile His Pro Ser Thr Ala Ser Thr Val Val Thr Pro Ala Ala Val
 245 250 255
 Leu Pro Gly Leu Ala Gln Val Ile Thr Ala Val Ser Ala Gln Gln Asn
 260 265 270

Ser	Asn	Leu	Ile	Pro	Lys	Val	Leu	Ile	Pro	Val	Asn	Ser	Ile	Pro	Thr	275	280	285
Tyr	Asn	Ala	Ala	Leu	Asp	Asn	Asn	Pro	Leu	Leu	Leu	Asn	Thr	Tyr	Asn	290	295	300
Lys	Phe	Pro	Tyr	Pro	Thr	Met	Ser	Glu	Ile	Thr	Val	Leu	Ser	Ala	Gln	305	310	315
Ala	Lys	Tyr	Thr	Glu	Glu	Gln	Ile	Lys	Ile	Trp	Phe	Ser	Ala	Gln	Arg	325	330	335
Leu	Lys	His	Gly	Val	Ser	Trp	Thr	Pro	Glu	Glu	Val	Glu	Glu	Ala	Arg	340	345	350
Arg	Lys	Gln	Phe	Asn	Gly	Thr	Val	His	Thr	Val	Pro	Gln	Thr	Ile	Thr	355	360	365
Val	Ile	Pro	Thr	His	Ile	Ser	Thr	Gly	Ser	Asn	Gly	Leu	Pro	Ser	Ile	370	375	380
Leu	Gln	Thr	Cys	Gln	Ile	Val	Gly	Gln	Pro	Gly	Leu	Val	Leu	Thr	Gln	385	390	395
Val	Ala	Gly	Thr	Asn	Thr	Leu	Pro	Val	Thr	Ala	Pro	Ile	Ala	Leu	Thr	405	410	415
Val	Ala	Gly	Val	Pro	Ser	Gln	Asn	Asn	Ile	Gln	Lys	Ser	Gln	Val	Pro	420	425	430
Ala	Ala	Gln	Pro	Thr	Ala	Glu	Thr	Lys	Pro	Ala	Thr	Ala	Ala	Val	Pro	435	440	445
Thr	Ser	Gln	Ser	Val	Lys	His	Glu	Thr	Ala	Leu	Val	Asn	Pro	Asp	Ser	450	455	460
Phe	Gly	Ile	Arg	Ala	Lys	Lys	Thr	Lys	Glu	Gln	Leu	Ala	Glu	Leu	Lys	465	470	475
Val	Ser	Tyr	Leu	Lys	Asn	Gln	Phe	Pro	His	Asp	Ser	Glu	Ile	Ile	Arg	485	490	495
Leu	Met	Lys	Ile	Thr	Gly	Leu	Thr	Lys	Gly	Glu	Ile	Lys	Lys	Trp	Phe	500	505	510
Ser	Asp	Thr	Arg	Tyr	Asn	Gln	Arg	Asn	Ser	Lys	Ser	Asn	Gln	Cys	Leu	515	520	525
His	Leu	Asn	Asn	Asp	Ser	Ser	Thr	Thr	Ile	Ile	Ile	Asp	Ser	Ser	Asp	530	535	540
Glu	Thr	Thr	Glu	Ser	Pro	Thr	Val	Gly	Thr	Ala	Gln	Pro	Lys	Gln	Ser	545	550	555
Trp	Asn	Pro	Phe	Pro	Asp	Phe	Thr	Pro	Gln	Lys	Phe	Lys	Glu	Lys	Thr	565	570	575

Ala	Glu	Gln	Leu	Arg	Val	Leu	Gln	Ala	Ser	Phe	Leu	Asn	Ser	Ser	Val	580	585	590	
Leu	Thr	Asp	Glu	Glu	Leu	Asn	Arg	Leu	Arg	Ala	Gln	Thr	Lys	Leu	Thr	595	600	605	
Arg	Arg	Glu	Ile	Asp	Ala	Trp	Phe	Thr	Glu	Lys	Lys	Lys	Ser	Lys	Ala	610	615	620	
Leu	Lys	Glu	Glu	Lys	Met	Glu	Ile	Asp	Glu	Ser	Asn	Ala	Gly	Ser	Ser	625	630	635	640
Lys	Glu	Glu	Ala	Gly	Glu	Thr	Ser	Pro	Ala	Asp	Glu	Ser	Gly	Ala	Pro	645	650	655	
Lys	Ser	Gly	Ser	Thr	Gly	Lys	Ile	Cys	Lys	Lys	Thr	Pro	Glu	Gln	Leu	660	665	670	
His	Met	Leu	Lys	Ser	Ala	Phe	Val	Arg	Thr	Gln	Trp	Pro	Ser	Pro	Glu	675	680	685	
Glu	Tyr	Asp	Lys	Leu	Ala	Lys	Glu	Ser	Gly	Leu	Ala	Arg	Thr	Asp	Ile	690	695	700	
Val	Ser	Trp	Phe	Gly	Asp	Thr	Arg	Tyr	Ala	Trp	Lys	Asn	Gly	Asn	Leu	705	710	715	720
Lys	Trp	Tyr	Tyr	Tyr	Tyr	Gln	Ser	Ala	Asn	Ser	Ser	Ser	Met	Asn	Gly	725	730	735	
Leu	Ser	Ser	Leu	Arg	Lys	Arg	Gly	Arg	Gly	Arg	Pro	Lys	Gly	Arg	Gly	740	745	750	
Arg	Gly	Arg	Pro	Arg	Gly	Arg	Pro	Arg	Gly	Ser	Lys	Arg	Ile	Asn	Asn	755	760	765	
Trp	Asp	Arg	Gly	Pro	Ser	Leu	Ile	Lys	Phe	Lys	Thr	Gly	Thr	Ala	Ile	770	775	780	
Leu	Lys	Asp	Tyr	Tyr	Leu	Lys	His	Lys	Phe	Leu	Asn	Glu	Gln	Asp	Leu	785	790	795	800
Asp	Glu	Leu	Val	Asn	Lys	Ser	His	Met	Gly	Tyr	Glu	Gln	Val	Arg	Glu	805	810	815	
Trp	Phe	Ala	Glu	Arg	Gln	Arg	Arg	Ser	Glu	Leu	Gly	Ile	Glu	Leu	Phe	820	825	830	
Glu	Glu	Asn	Glu	Glu	Glu	Asp	Glu	Val	Ile	Asp	Asp	Gln	Glu	Glu	Asp	835	840	845	
Glu	Glu	Glu	Thr	Asp	Asp	Ser	Asp	Thr	Trp	Glu	Pro	Pro	Arg	His	Val	850	855	860	
Lys	Arg	Lys	Leu	Ser	Lys	Ser	Asp	Asp								865	870		